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SEQUENCE LISTING

<110> Haroche, Julien
Allignet, Jeanine
El Solh, Nevine

<120> DETECTION OF A GENE, vatD, ENCODING AN ACETYLTRANSFERASE
INACTIVATING STREPTOGRAMIN

<130> 03495.0193

<140>

<141>

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 213

<212> PRT

<213> Enterococcus faecium

<400> 1

Met	Thr	Ile	Pro	Asp	Ala	Asn	Ala	Ile	Tyr	His	Asn	Ser	Ala	Ile	Lys
1				5					10					15	
Glu	Val	Val	Phe	Ile	Lys	Asn	Val	Ile	Lys	Ser	Pro	Asn	Ile	Glu	Ile
			20					25					30		
Gly	Asp	Tyr	Thr	Tyr	Tyr	Asp	Asp	Pro	Val	Asn	Pro	Thr	Asp	Phe	Glu
	35					40					45				
Lys	His	Val	Thr	His	His	Tyr	Glu	Phe	Leu	Gly	Asp	Lys	Leu	Ile	Ile
	50					55					60				
Gly	Lys	Phe	Cys	Ser	Leu	Ala	Ser	Gly	Ile	Glu	Phe	Ile	Met	Asn	Gly
65					70					75					80
Ala	Asn	His	Val	Met	Lys	Gly	Ile	Ser	Thr	Tyr	Pro	Phe	Asn	Ile	Leu
				85					90					95	
Gly	Gly	Asp	Trp	Gln	Gln	Tyr	Thr	Pro	Glu	Leu	Thr	Asp	Leu	Pro	Leu
		100						105					110		
Lys	Gly	Asp	Thr	Val	Val	Gly	Asn	Asp	Val	Trp	Phe	Gly	Gln	Asn	Val
		115					120					125			
Thr	Val	Leu	Pro	Gly	Val	Lys	Ile	Gly	Asp	Gly	Ala	Ile	Ile	Gly	Ala
	130					135					140				
Asn	Ser	Val	Val	Thr	Lys	Asp	Val	Ala	Pro	Tyr	Thr	Ile	Val	Gly	Gly
145					150					155				160	
Asn	Pro	Ile	Gln	Leu	Ile	Gly	Pro	Arg	Phe	Glu	Pro	Glu	Val	Ile	Gln
			165						170					175	

Ala Leu Glu Asn Leu Ala Trp Trp Asn Lys Asp Ile Glu Trp Ile Thr
 180 185 190

Ala Asn Val Pro Lys Leu Met Gln Thr Thr Pro Thr Leu Glu Leu Ile
 195 200 205

Asn Ser Leu Met Glu
 210

<210> 2
 <211> 642
 <212> DNA
 <213> Enterococcus faecium

<400> 2
 atgactatac ctgacgcaaa tgcaatctat cataactcag ccatcaaaga ggttgtcttt 60
 atcaagaacg tgatcaaaag tcccaatatt gaaattgggg actacaccta ttatgatgac 120
 ccagtaaadc ccaccgattt tgagaaacac gttacccatc actatgaatt tctaggcgac 180
 aaattaatca tcggtaaatt ttgttctctc gccagtggca ttgaatttat catgaacggt 240
 gccaacacg taatgaaagg tatttcgact tatccattta atatattagg tggcgattgg 300
 caacaatata ctctgaact gactgatttg ccgttgaaag gtgatactgt agtcggaaat 360
 gacgtgtggt ttgggcaaaa tgtgaccgtc ctaccaggcg taaaaatagg tgacggtgcc 420
 attatcggag caaatagtgt tgtaacaaaa gacgtcgtc catatacaat tgtcgggtggc 480
 aatccaattc aactcatcgg accaagattt gaaccggaag ttattcaagc attagaaaat 540
 ctggcatggt ggaataaaga tattgaatgg ataactgcta atgttcctaa actaatgcaa 600
 acaacacca cacttgaatt gataaacagt ttaatggaaa aa 642

<210> 3
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 3
 caatattgga attcgggact acacc 25

<210> 4
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 4
 ctgtttatga attcaagtgt gg 22

<210> 5
 <211> 7
 <212> PRT
 <213> Enterococcus faecium

<400> 5
 Ile Met Asn Gly Ala Asn His
 1 5

<210> 6
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <223> "n" bases may be a, t, c or g

<400> 6
 athatgaayg cnaaycay

18

<210> 7
 <211> 5
 <212> PRT
 <213> Enterococcus faecium

<400> 7
 Gly Asn Asp Val Trp
 1 5

<210> 8
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <223> "n" bases may be a, t, c or g

<400> 8
 ccanacrter ttncc

15

<210> 9
 <211> 8
 <212> PRT
 <213> Enterococcus faecium

<400> 9
 Ala Asn Ala Ile Tyr His Asn Ser
 1 5

<210> 10
 <211> 24
 <212> DNA

<213> Enterococcus faecium

<400> 10

gcaaagcaa tctatcataa ctca

24

<210> 11

<211> 9

<212> PRT

<213> Enterococcus faecium

<400> 11

Met Gln Thr Thr Pro Thr Leu Glu Leu

1

5

<210> 12

<211> 27

<212> DNA

<213> Enterococcus faecium

<400> 12

atgcaaaca caccacact tgaattg

27

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

tagaaagaat tcagtgattg tgg

23

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

ggattcacta aatagtaaag gccgtg

26

<210> 15

<211> 840

<212> DNA

<213> Enterococcus faecium

<400> 15

aaatttaggc gcacaaaaag aaagagtgtg acaaaacatg gttatgctac atgtttaagg 60
taaaaatagt tatgtcacia ctacttattt ttttaccocaa tcttctagac tataattaaa 120
attaaataac tcaattcgga ggtactaacc tgactatacc tgacgcaaat gcaatctatc 180

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ataactcagc catcaaagag gttgacttta tcaagaacgt gatcaaaaagt cccaatattg 240
aaattgggga ctacacctat tatgatgacc cagtaaatcc caccgatttt gagaaacacg 300
ttacccatca ctatgaattt ctaggcgaca aattaatcat cggtaaattt tgttctctcg 360
ccagtggcat tgaattttatc atgaacgggtg ccaaccacgt aatgaaaggt atttcgactt 420
atccatttaa tatattaggt ggcgattggc aacaatacac tcctgaactg actgatttgc 480
cgttgaaagg tgatactgta gtcgggaaatg acgtgtgggtt tgggcaaaat gtgaccgtcc 540
taccaggcgt aaaaataggt gacggtgcca ttatcggagc aaatagtgtt gtaacaaaag 600
acgtcgctcc atatacaatt gtcggtgcca atccaattca actcatcgga ccaagatttg 660
aaccggaagt tattcaagca ttagaaaatc tggcatgggtg gaataaagat attgaatgga 720
taactgctaa tgttcctaaa ctaatgcaaa caacacccac acttgaattg ataaacagtt 780
taatggaaaa ataaaaacaa aaaagccgtg caagcaatcc aaaaatgatt gtttacacgg 840

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<210> 16
<211> 44
<212> DNA
<213> Enterococcus faecium

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<400> 16
tgtcacaact acttattttt ttaccaatc ttctagacta taat 44

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<210> 17
<211> 1080
<212> DNA
<213> Enterococcus faecium

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<220>
<221> CDS
<222> (271) .. (912)

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<400> 17
ccctttaag agggctttta tatattaatc acaaatcact tatcacaat cacaagtgat 60

ttgtgattgt tgatgataaa ataagaataa gaagaaatag aaagaagtga gtgattgtgg 120

gaaatttagg cgcacaaaaa gaaagagtgt gacaaaacat ggttatgcta catgtttaag 180

gtaaaaatag ttatgtcaca actacttatt tttttaccca atcttctaga ctataattaa 240

aattaaataa ctcaattcgg aggtactaac atg act ata cct gac gca aat gca 294
                Met Thr Ile Pro Asp Ala Asn Ala
                1                5

atc tat cat aac tca gcc atc aaa gag gtt gtc ttt atc aag aac gtg 342
Ile Tyr His Asn Ser Ala Ile Lys Glu Val Val Phe Ile Lys Asn Val
    10                15                20

atc aaa agt ccc aat att gaa att ggg gac tac acc tat tat gat gac 390
Ile Lys Ser Pro Asn Ile Glu Ile Gly Asp Tyr Thr Tyr Tyr Asp Asp
    25                30                35                40

cca gta aat ccc acc gat ttt gag aaa cac gtt acc cat cac tat gaa 438
Pro Val Asn Pro Thr Asp Phe Glu Lys His Val Thr His His Tyr Glu
    45                50                55

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ttt cta ggc gac aaa tta atc atc ggt aaa ttt tgt tct ctc gcc agt 486
 Phe Leu Gly Asp Lys Leu Ile Ile Gly Lys Phe Cys Ser Leu Ala Ser
 60 65 70

ggc att gaa ttt atc atg aac ggt gcc aac cac gta atg aaa ggt att 534
 Gly Ile Glu Phe Ile Met Asn Gly Ala Asn His Val Met Lys Gly Ile
 75 80 85

tcg act tat cca ttt aat ata tta ggt ggc gat tgg caa caa tac act 582
 Ser Thr Tyr Pro Phe Asn Ile Leu Gly Gly Asp Trp Gln Gln Tyr Thr
 90 95 100

cct gaa ctg act gat ttg ccg ttg aaa ggt gat act gta gtc gga aat 630
 Pro Glu Leu Thr Asp Leu Pro Leu Lys Gly Asp Thr Val Val Gly Asn
 105 110 115 120

gac gtg tgg ttt ggg caa aat gtg acc gtc cta cca ggc gta aaa ata 678
 Asp Val Trp Phe Gly Gln Asn Val Thr Val Leu Pro Gly Val Lys Ile
 125 130 135

ggt gac ggt gcc att atc gga gca aat agt gtt gta aca aaa gac gtc 726
 Gly Asp Gly Ala Ile Ile Gly Ala Asn Ser Val Val Thr Lys Asp Val
 140 145 150

gct cca tat aca att gtc ggt ggc aat cca att caa ctc atc gga cca 774
 Ala Pro Tyr Thr Ile Val Gly Gly Asn Pro Ile Gln Leu Ile Gly Pro
 155 160 165

aga ttt gaa ccg gaa gtt att caa gca tta gaa aat ctg gca tgg tgg 822
 Arg Phe Glu Pro Glu Val Ile Gln Ala Leu Glu Asn Leu Ala Trp Trp
 170 175 180

aat aaa gat att gaa tgg ata act gct aat gtt cct aaa cta atg caa 870
 Asn Lys Asp Ile Glu Trp Ile Thr Ala Asn Val Pro Lys Leu Met Gln
 185 190 195 200

aca aca ccc aca ctt gaa ttg ata aac agt tta atg gaa aaa 912
 Thr Thr Pro Thr Leu Glu Leu Ile Asn Ser Leu Met Glu Lys
 205 210

taaaaacaaa aaagccgtgc aagcaatcca aaaatgattg tttacacggc ctttactatt 972

tagtgaatcc aatttattaa taatagatat gatataccag taaaaaatac actagccacc 1032

tctggcggta ctctactcgt atatttttatt tacgaccttc tgatgata 1080

<210> 18

<211> 214

<212> PRT

<213> Enterococcus faecium

<400> 18

Met Thr Ile Pro Asp Ala Asn Ala Ile Tyr His Asn Ser Ala Ile Lys
 1 5 10 15

Glu Val Val Phe Ile Lys Asn Val Ile Lys Ser Pro Asn Ile Glu Ile
 20 25 30

Gly	Asp	Tyr	Thr	Tyr	Tyr	Asp	Asp	Pro	Val	Asn	Pro	Thr	Asp	Phe	Glu
35						40						45			
Lys	His	Val	Thr	His	His	Tyr	Glu	Phe	Leu	Gly	Asp	Lys	Leu	Ile	Ile
50						55				60					
Gly	Lys	Phe	Cys	Ser	Leu	Ala	Ser	Gly	Ile	Glu	Phe	Ile	Met	Asn	Glu
65				70						75				80	
Ala	Asn	His	Val	Met	Lys	Gly	Ile	Ser	Thr	Tyr	Pro	Phe	Asn	Ile	Leu
				85				90						95	
Gly	Gly	Asp	Trp	Gln	Gln	Tyr	Thr	Pro	Glu	Leu	Thr	Asp	Leu	Pro	Leu
		100						105				110			
Lys	Gly	Asp	Thr	Val	Val	Gly	Asn	Asp	Val	Trp	Phe	Gly	Gln	Asn	Val
		115				120						125			
Thr	Val	Leu	Pro	Gly	Val	Lys	Ile	Gly	Asp	Gly	Ala	Ile	Ile	Gly	Ala
130						135				140					
Asn	Ser	Val	Val	Thr	Lys	Asp	Val	Ala	Pro	Tyr	Thr	Ile	Val	Gly	Gly
145				150						155				160	
Asn	Pro	Ile	Gln	Leu	Ile	Gly	Pro	Arg	Phe	Glu	Pro	Glu	Val	Ile	Gln
				165				170						175	
Ala	Leu	Glu	Asn	Leu	Ala	Trp	Trp	Asn	Lys	Asp	Ile	Glu	Trp	Ile	Thr
		180						185				190			
Ala	Asn	Val	Pro	Lys	Leu	Met	Gln	Thr	Thr	Pro	Thr	Leu	Glu	Leu	Ile
195						200						205			
Asn	Ser	Leu	Met	Glu	Lys										
210															

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<210> 19
<211> 219
<212> PRT
<213> Unknown Organism
```

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<220>
<223> Description of Unknown Organism: acetyltransferase
      enzyme
```

<400> 19
Leu Asn Leu Asn Asn Asp His Gly Pro Asp Pro Glu Asn Ile Leu Pro
1 5 10 15
Ile Lys Gly Asn Arg Asn Leu Gln Phe Ile Lys Pro Thr Ile Thr Asn
20 25 30
Glu Asn Ile Leu Val Gly Glu Tyr Ser Tyr Tyr Asp Ser Lys Arg Gly
35 40 45

Glu Ser Phe Glu Asp Gln Val Leu Tyr His Tyr Glu Val Ile Gly Asp
 50 55 60
 Lys Leu Ile Ile Gly Arg Phe Cys Ser Ile Gly Pro Gly Thr Thr Phe
 65 70 75 80
 Ile Met Asn Gly Ala Asn His Arg Met Asp Gly Ser Thr Tyr Pro Phe
 85 90 95
 His Leu Phe Arg Met Gly Trp Glu Lys Tyr Met Pro Ser Leu Lys Asp
 100 105 110
 Leu Pro Leu Lys Gly Asp Ile Glu Ile Gly Asn Asp Val Trp Ile Gly
 115 120 125
 Arg Asp Val Thr Ile Met Pro Gly Val Lys Ile Gly Asp Gly Ala Ile
 130 135 140
 Ile Ala Ala Glu Ala Val Val Thr Lys Asn Val Ala Pro Tyr Ser Ile
 145 150 155 160
 Val Gly Gly Asn Pro Leu Lys Phe Ile Arg Lys Arg Phe Ser Asp Gly
 165 170 175
 Val Ile Glu Glu Trp Leu Ala Leu Gln Trp Trp Asn Leu Asp Met Lys
 180 185 190
 Ile Ile Asn Glu Asn Leu Pro Phe Ile Ile Asn Gly Asp Ile Glu Met
 195 200 205
 Leu Lys Arg Lys Arg Lys Leu Leu Asp Asp Thr
 210 215

<210> 20

<211> 212

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: acetyltransferase
enzyme

<400> 20

Met Lys Trp Gln Asn Gln Gln Gly Pro Asn Pro Glu Glu Ile Tyr Pro
 1 5 10 15
 Ile Glu Gly Asn Lys His Val Gln Phe Ile Lys Pro Ser Ile Thr Lys
 20 25 30
 Pro Asn Ile Leu Val Gly Glu Tyr Ser Tyr Tyr Asp Ser Lys Asp Gly
 35 40 45
 Glu Ser Phe Glu Ser Gln Val Leu Tyr His Tyr Glu Leu Ile Gly Asp
 50 55 60
 Lys Leu Ile Leu Gly Lys Phe Cys Ser Ile Gly Pro Gly Thr Thr Phe
 65 70 75 80

[illegible]

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<210> 21
<211> 209
<212> PRT
<213> Unknown Organism
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<220>
<223> Description of Unknown Organism: acetyltransferase
      enzyme
```

```

<400> 21
Met Gly Pro Asn Pro Met Lys Met Tyr Pro Ile Glu Gly Asn Lys Ser
  1             5             10             15
Val Gln Phe Ile Lys Pro Ile Leu Glu Lys Leu Glu Asn Val Glu Val
          20             25             30
Gly Glu Tyr Ser Tyr Tyr Asp Ser Lys Asn Gly Glu Thr Phe Asp Lys
      35             40             45
Gln Ile Leu Tyr His Tyr Pro Ile Leu Asn Asp Lys Leu Lys Ile Gly
  50             55             60
Lys Phe Cys Ser Ile Gly Pro Gly Val Thr Ile Ile Met Asn Gly Ala
  65             70             75             80
Asn His Arg Met Asp Gly Ser Thr Tyr Pro Phe Asn Leu Phe Gly Asn
      85             90             95

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Gly Trp Glu Lys His Met Pro Lys Leu Asp Gln Leu Pro Ile Lys Gly
 100 105 110
 Asp Thr Ile Ile Gly Asn Asp Val Trp Ile Gly Lys Asp Val Val Ile
 115 120 125
 Met Pro Gly Val Lys Ile Gly Asp Gly Ala Ile Val Ala Ala Asn Ser
 130 135 140
 Val Val Val Lys Asp Ile Ala Pro Tyr Met Leu Ala Gly Gly Asn Pro
 145 150 155 160
 Ala Asn Glu Ile Lys Gln Arg Phe Asp Gln Asp Thr Ile Asn Gln Leu
 165 170 175
 Leu Asp Ile Lys Trp Trp Asn Trp Pro Ile Asp Ile Ile Asn Glu Asn
 180 185 190
 Ile Asp Lys Ile Leu Asp Asn Ser Ile Ile Arg Glu Val Ile Trp Lys
 195 200 205
 Lys

<210> 22
 <211> 212
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: acetyltransferase
 enzyme

<400> 22
 Met Lys Tyr Gly Pro Asp Pro Asn Ser Ile Tyr Pro His Glu Glu Ile
 1 5 10 15
 Lys Ser Val Cys Phe Ile Lys Asn Thr Ile Thr Asn Pro Asn Ile Ile
 20 25 30
 Val Gly Asp Tyr Thr Tyr Tyr Ser Asp Val Asn Gly Ala Glu Lys Phe
 35 40 45
 Glu Glu His Val Thr His His Tyr Glu Phe Arg Gly Asp Lys Leu Val
 50 55 60
 Ile Gly Lys Phe Cys Ala Ile Ala Glu Gly Ile Glu Phe Ile Met Asn
 65 70 75 80
 Gly Ala Asn His Arg Met Asn Ser Ile Thr Thr Tyr Pro Phe Asn Ile
 85 90 95
 Met Gly Asn Gly Trp Glu Lys Ala Thr Pro Ser Leu Glu Asp Leu Pro
 100 105 110
 Phe Lys Gly Asp Thr Val Val Gly Asn Asp Val Trp Ile Gly Gln Asn
 115 120 125

Val Thr Val Met Pro Gly Ile Gln Ile Gly Asp Gly Ala Ile Val Ala
130 135 140

Ala Asn Ser Val Val Thr Lys Asp Val Pro Pro Tyr Arg Ile Ile Gly
145 150 155 160

Gly Asn Pro Ser Arg Ile Ile Lys Lys Arg Phe Glu Asp Glu Leu Ile
165 170 175

Asp Tyr Leu Leu Gln Ile Lys Trp Trp Asp Trp Ser Ala Gln Lys Ile
180 185 190

Phe Ser Asn Leu Glu Thr Leu Cys Ser Ser Asp Leu Glu Lys Ile Lys
195 200 205

Ser Ile Arg Asp
210